Analysis of target cell models

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Overview

This document goes over the results the target cell analysis. There are three analyses, in each of these analyses β and the starting time (start_time or t_0) were optimized to each infant's episode.

1. Expansion model fit - by analyzing the expansion portion only we can estimate R0 during the exponential phase.
2. Target cell fits for the entirety of the episode including transition and clearance phase.
3. Target cell fit profiling over a range of mu. In this analysis we also fitted δ.

The raw results come from fits using initial values drawn from latin hypercube. For this analysis, we restrict the best fit set for each infant (for each given mu when it varies).

Expansion data analysis

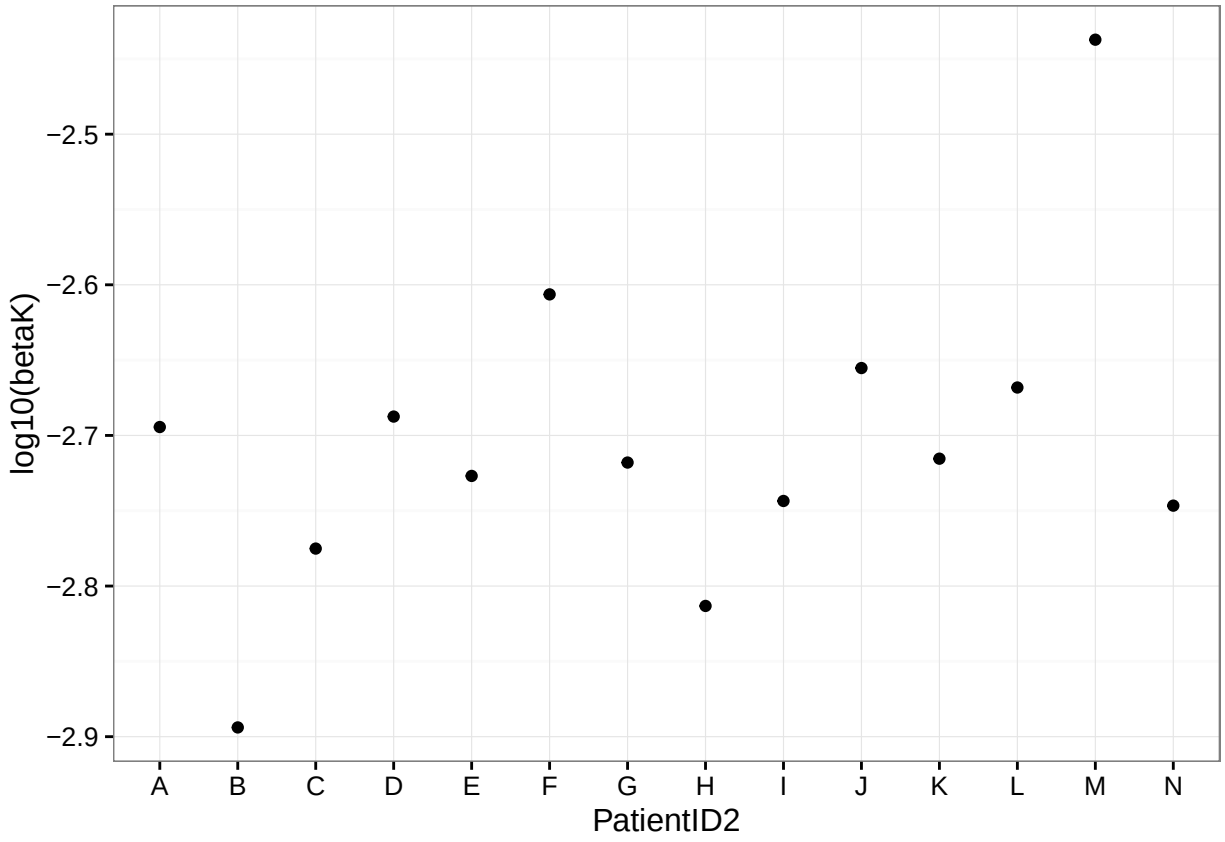
β is rescaled by K (S_0) and called betaK

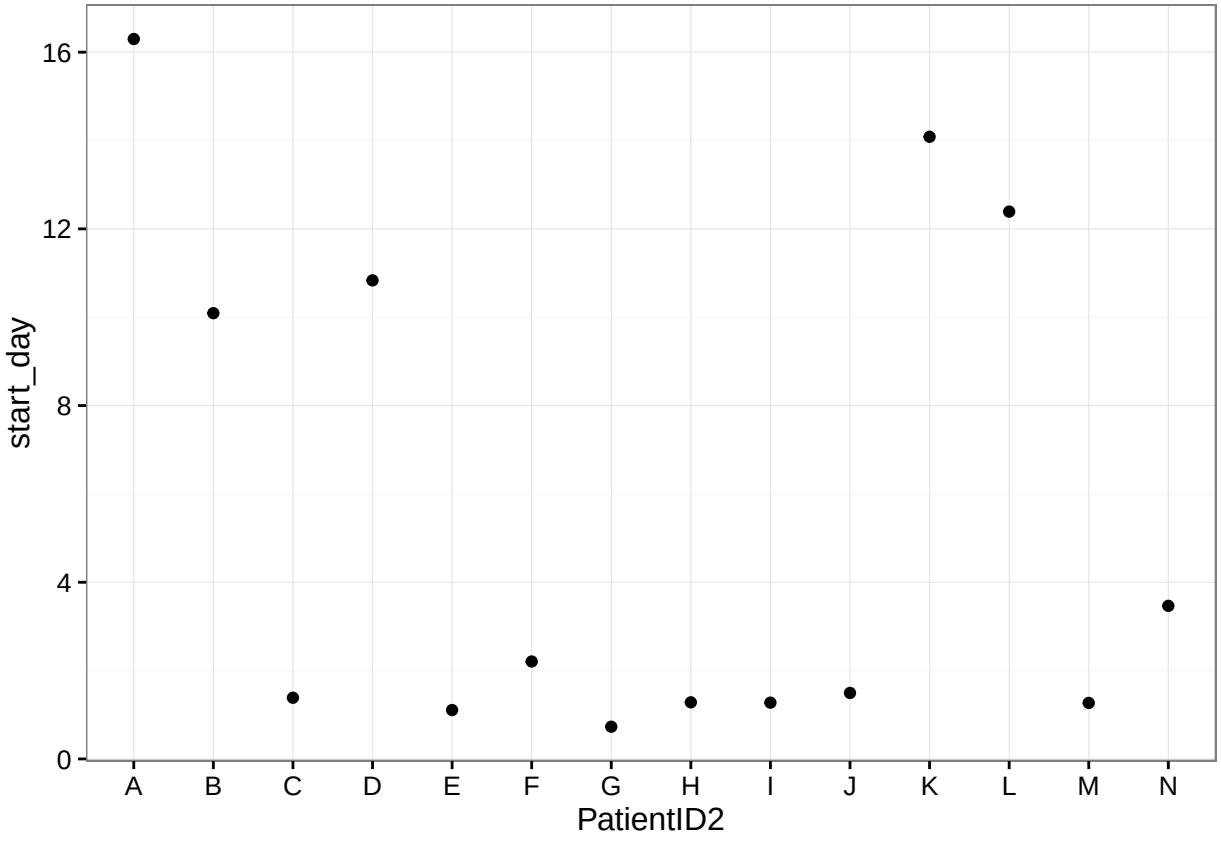
Look at best fit parameters

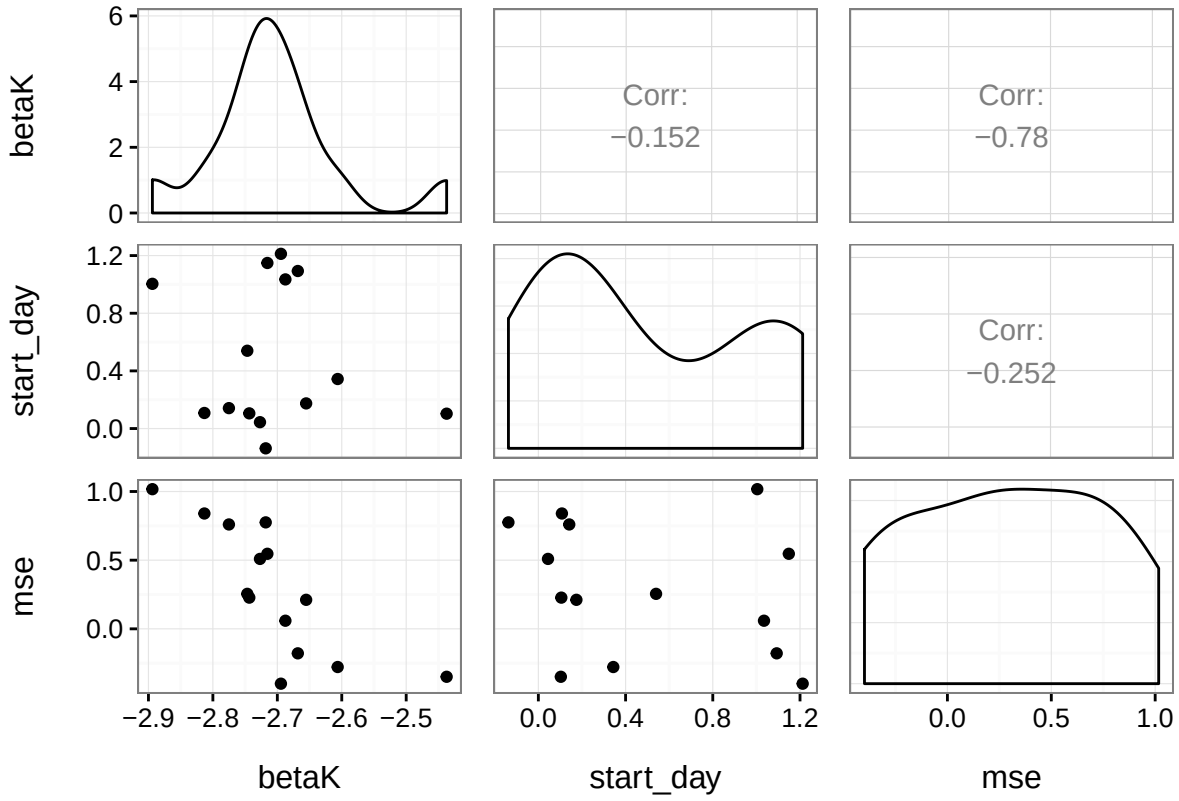
	PatientID2	start_day	mse	R0	betaKx1000
1	A	16.30	0.40	1.72	2.02
2	B	10.09	10.40	1.09	1.28
3	C	1.39	5.76	1.43	1.68
4	D	10.83	1.15	1.75	2.05
5	E	1.11	3.23	1.59	1.88
6	F	2.21	0.53	2.10	2.48
7	G	0.73	5.96	1.63	1.91
8	H	1.28	6.92	1.31	1.54
9	I	1.27	1.69	1.53	1.81
10	J	1.49	1.63	1.88	2.21
11	K	14.08	3.52	1.64	1.93
12	L	12.39	0.66	1.82	2.15
13	M	1.27	0.45	3.11	3.65
14	N	3.47	1.80	1.52	1.79

Table 1: Supplementary Table - Fits from expansion phase analysis

Look at correlation between features



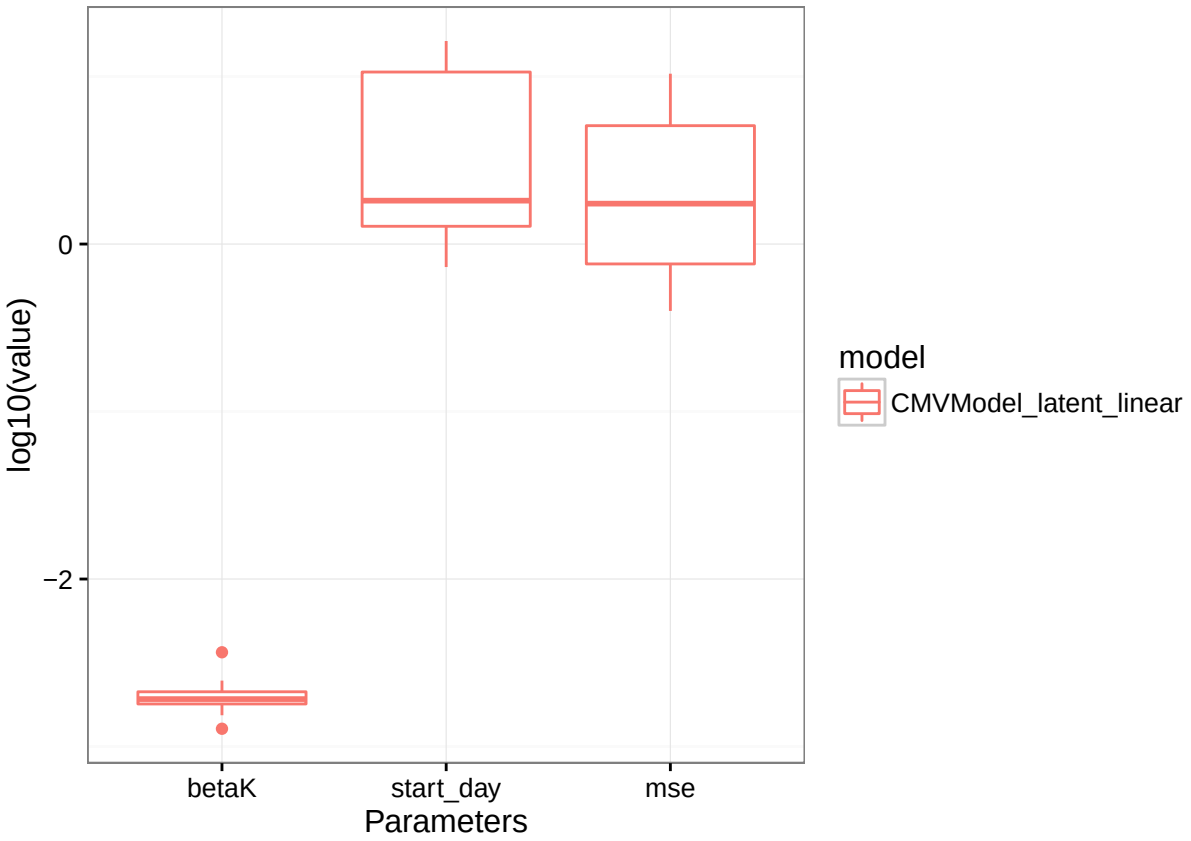

start_day
16
12
8
4
0
A
B
C
D
E
F
G
H
I
J
K
L
M
N
PatientID2


betaK
start_day
mse
Corr:
−0.152
Corr:
−0.78
Corr:
−0.252
6
4
2
0
1.2
0.8
0.4
0.0
1.0
0.5
0.0
−2.9
−2.8
−2.7
−2.6
−2.5
0.0
0.4
0.8
1.2
0.0
0.5
1.0
betaK
start_day
mse

Simulate the model with the best fits

Look at parameters by person

Note: this section saves a pdf with the fits and parameter values for each infant in `results_figures/base_model_fits.pdf`



Looking at total epithelial population

The model does not predict substantial decay in the susceptible population during the expansion phase, which validates our assumption about utilizing this portion of the data to inform R0. It also does not predict a loss in epithelial cells in general: this is likely from the assumption that μ replenishes the S pretty quickly.

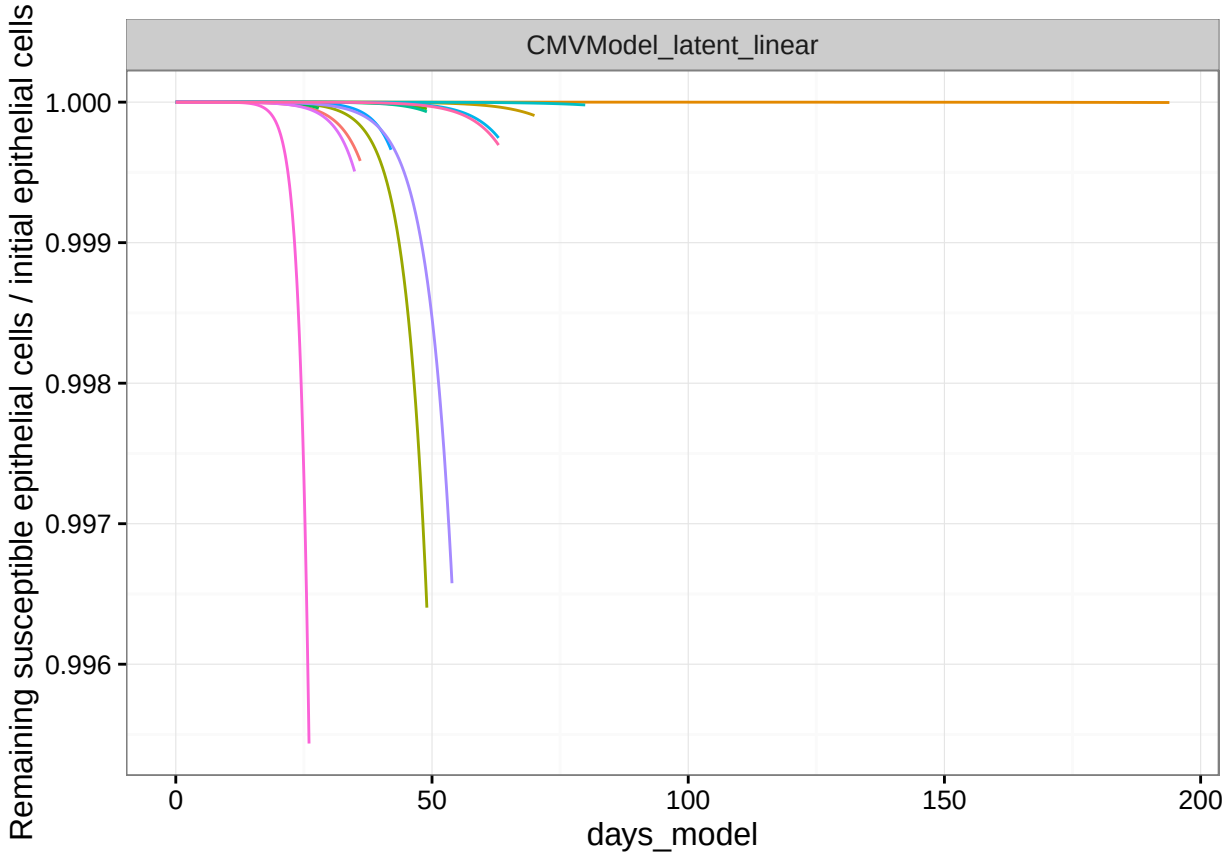


Figure 1: Depletion of S and total cells ($S+L+I$) is limited during expansion phase under best fit parameters

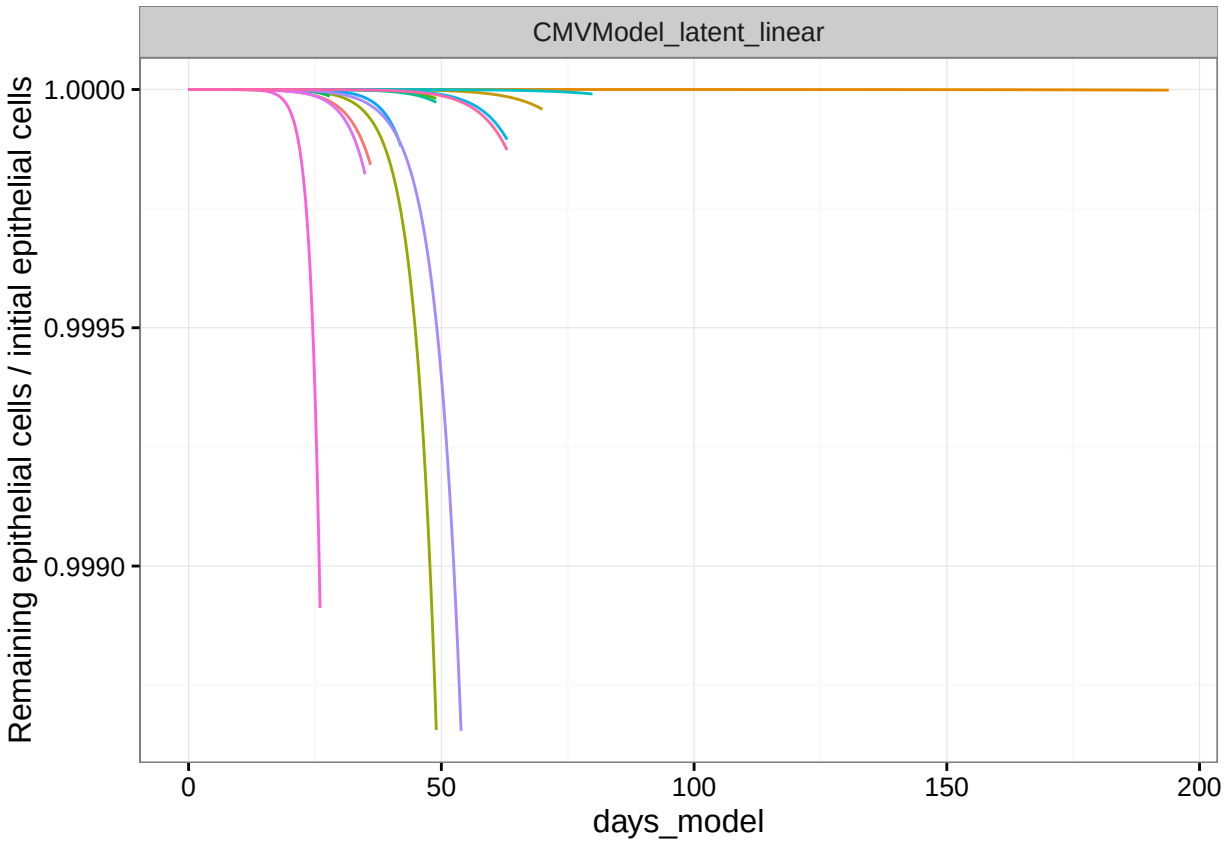
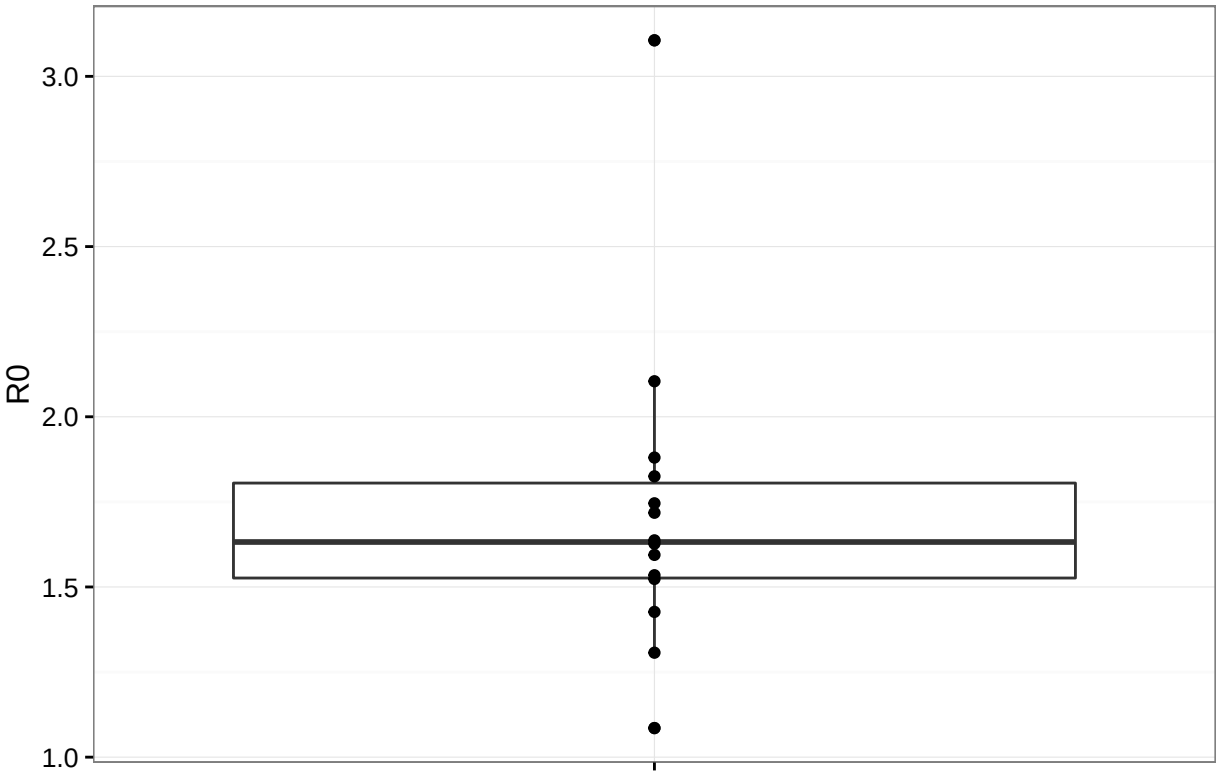


Figure 2: Depletion of S and total cells ($S+L+I$) is limited during expansion phase under best fit parameters

R0



Target cell model with biologically fixed parameters

Here $\mu = 1/4.5$ and $\delta = 0.77$. This model does a terrible job of recapitulating of fitting the data.

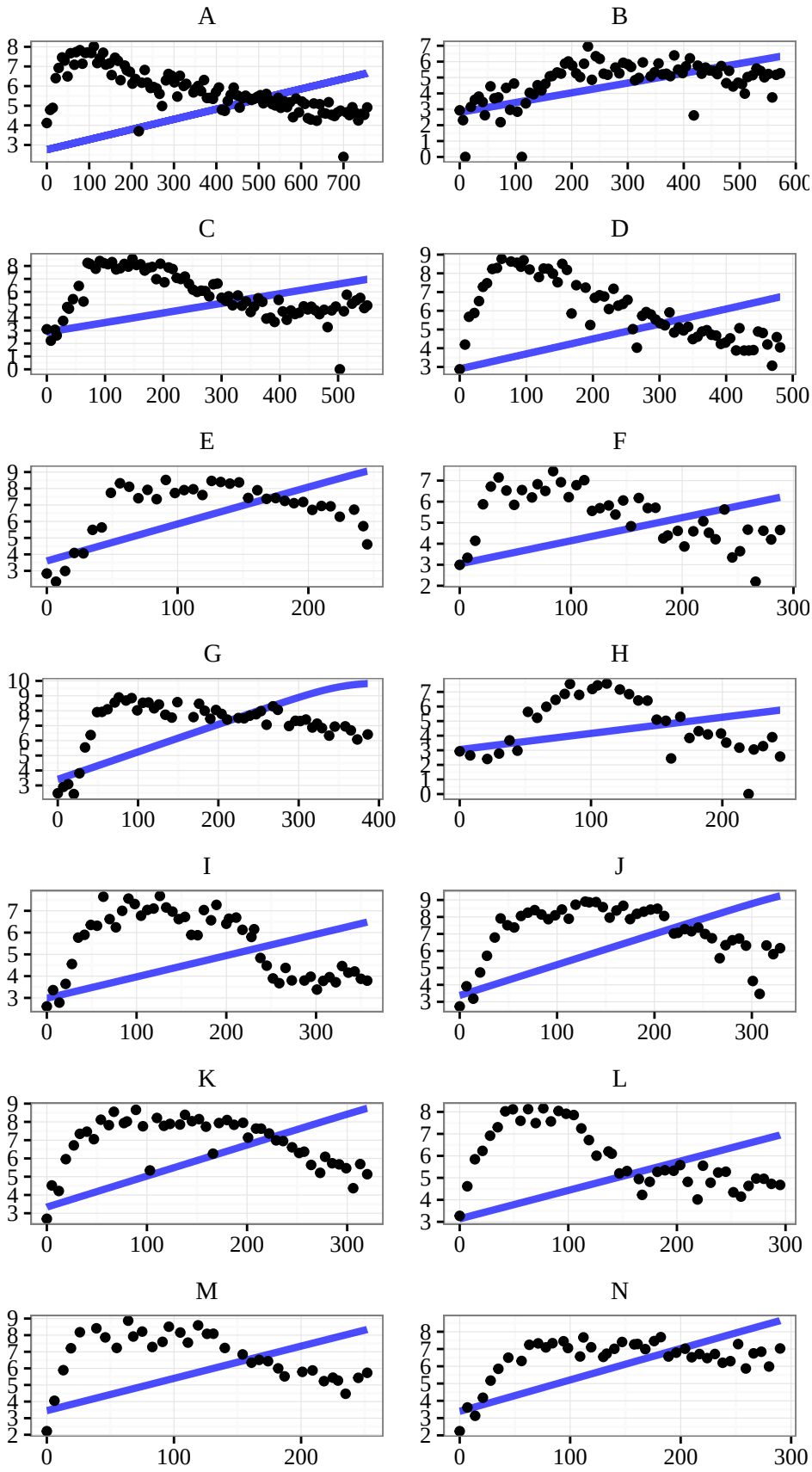
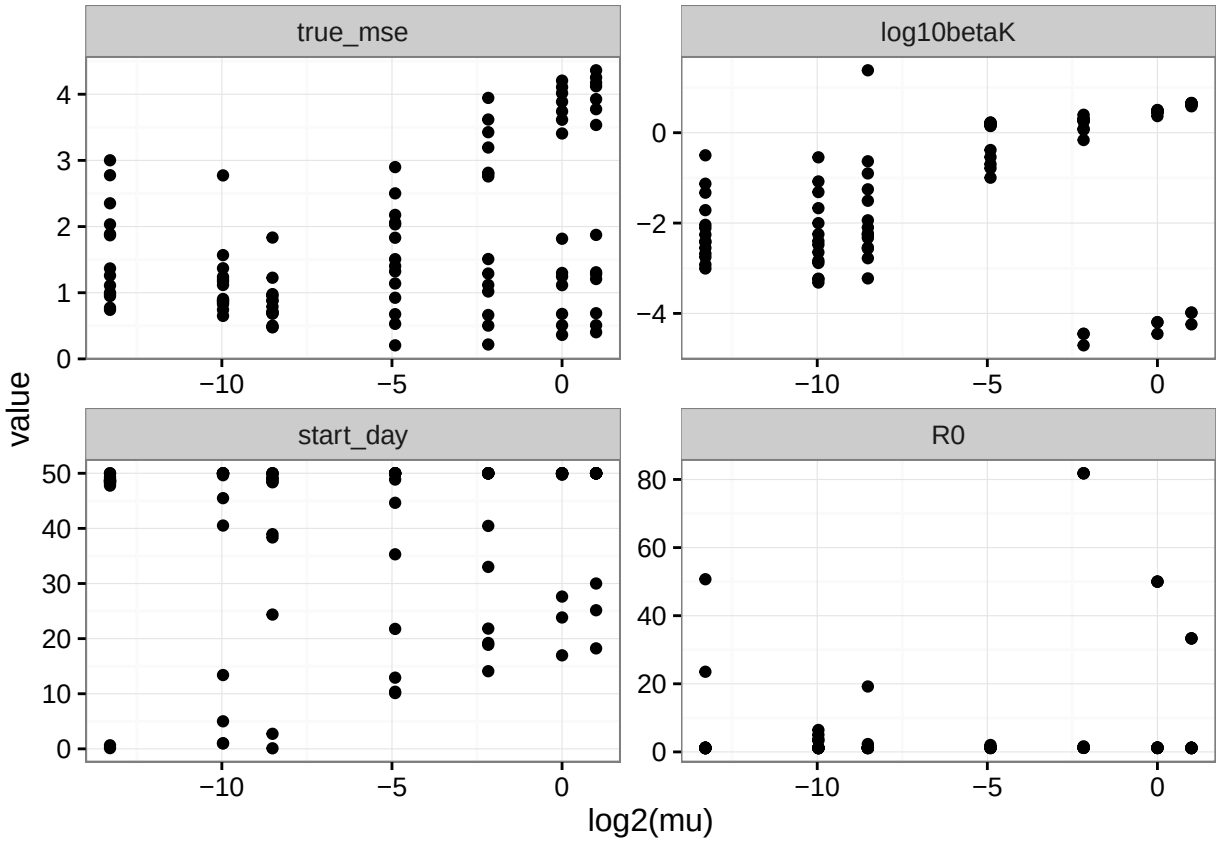


Figure 3: Target cell model with fixed delta and mu does poorly

Target cell model with varying μ

Look at parameter fits

Compare parameter fits across μ values



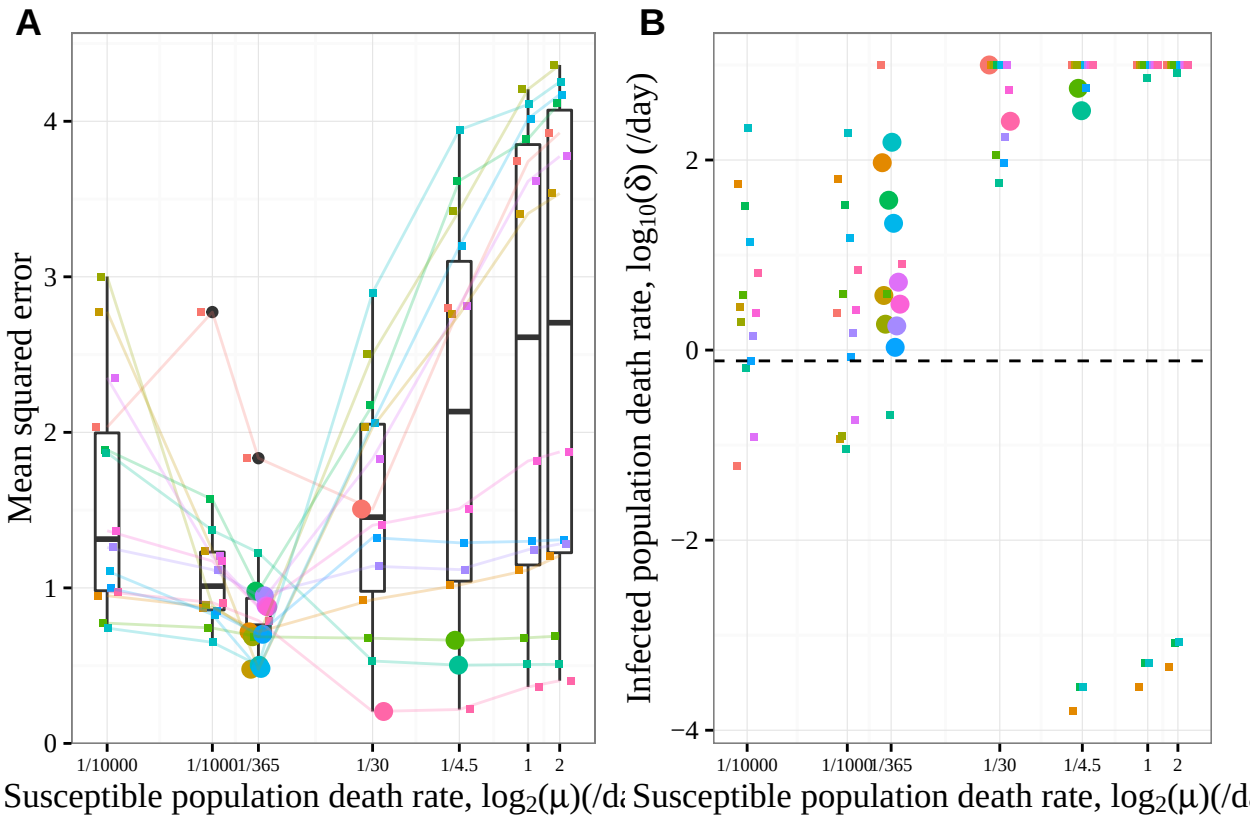
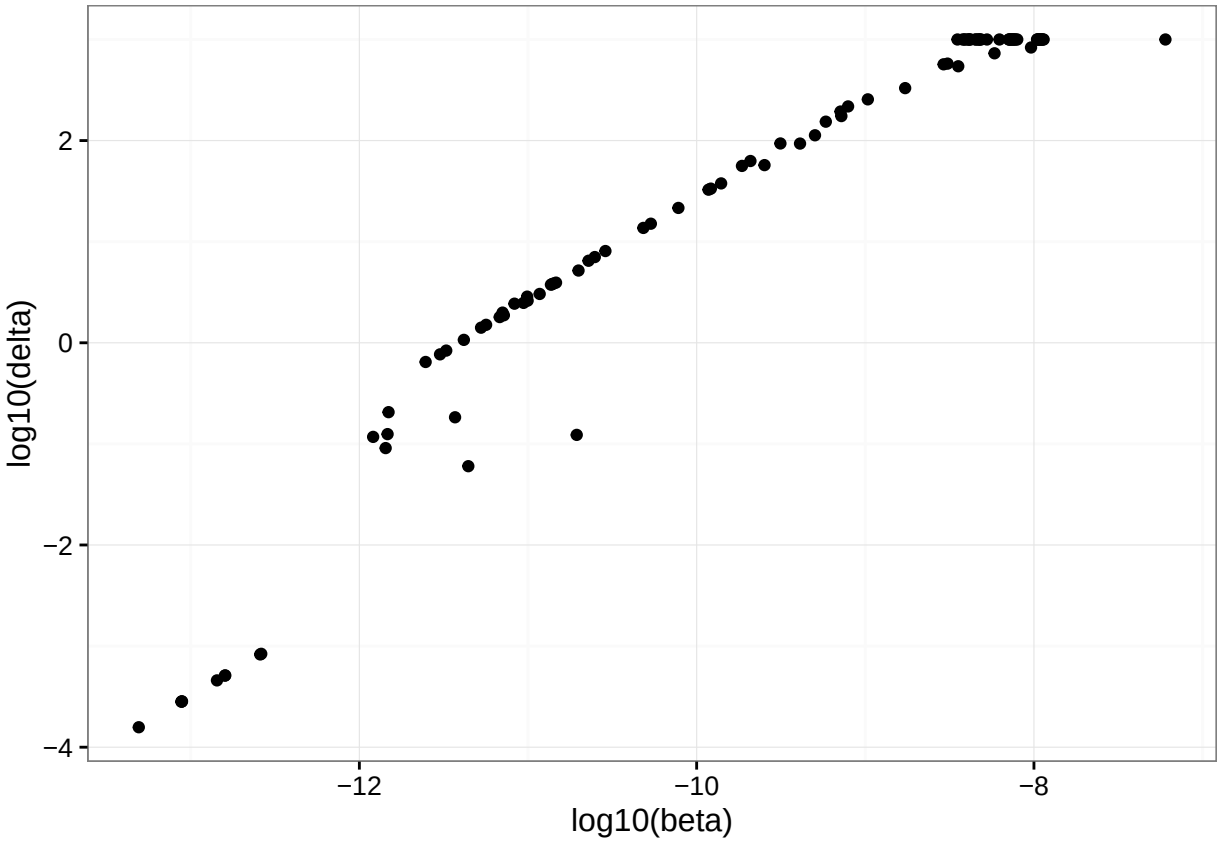


Figure 4: Main parameter effects by mu

β **vs** δ



Episode fits across μ

This model does a better job of capturing the data.

Loss of epithelial cells during model simulation

Substantial loss of epithelial population not consistent with the etiology of CMV infection.

Save output data and figures for supplement.

See code for this.

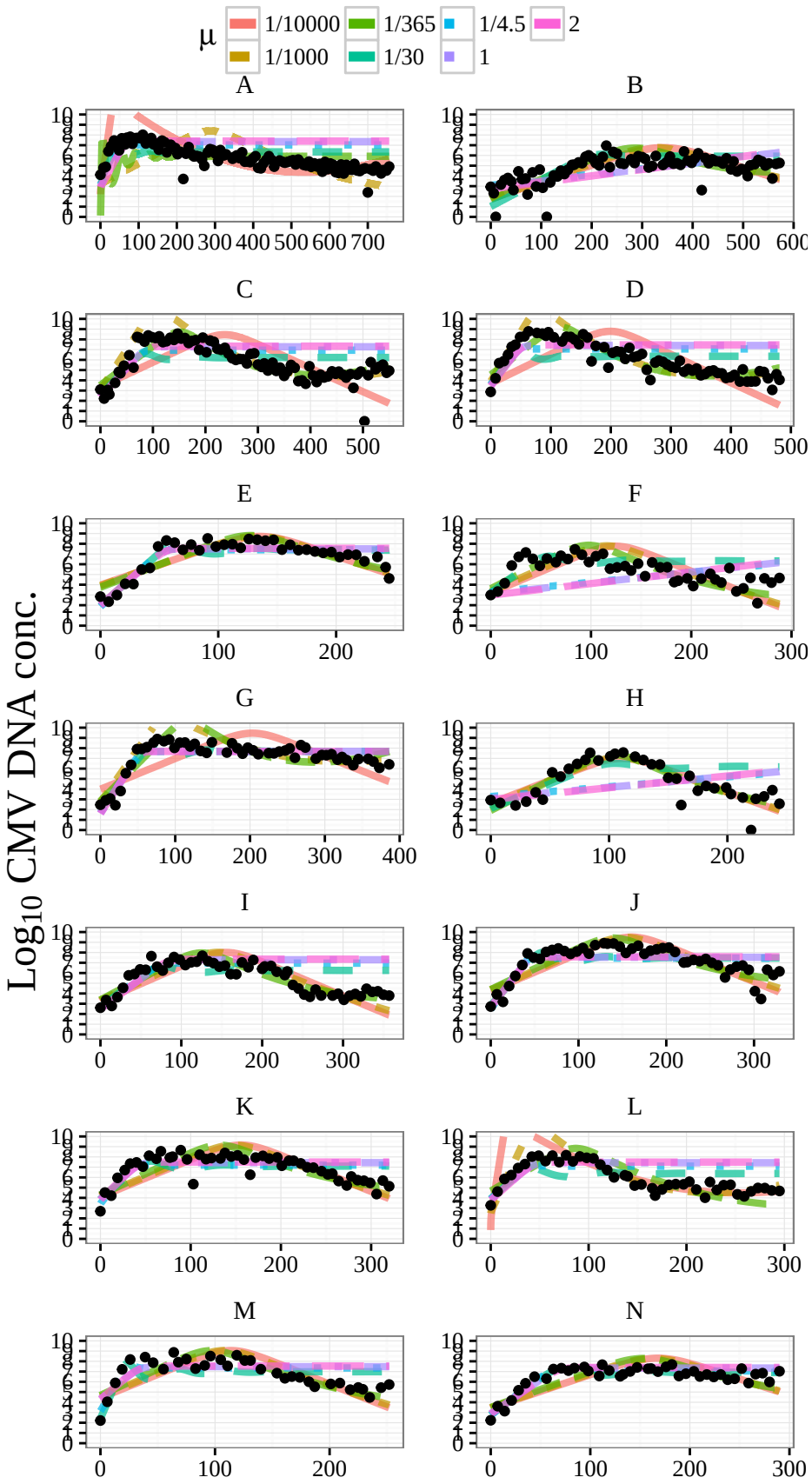


Figure 5: Best Target cell fits by mu

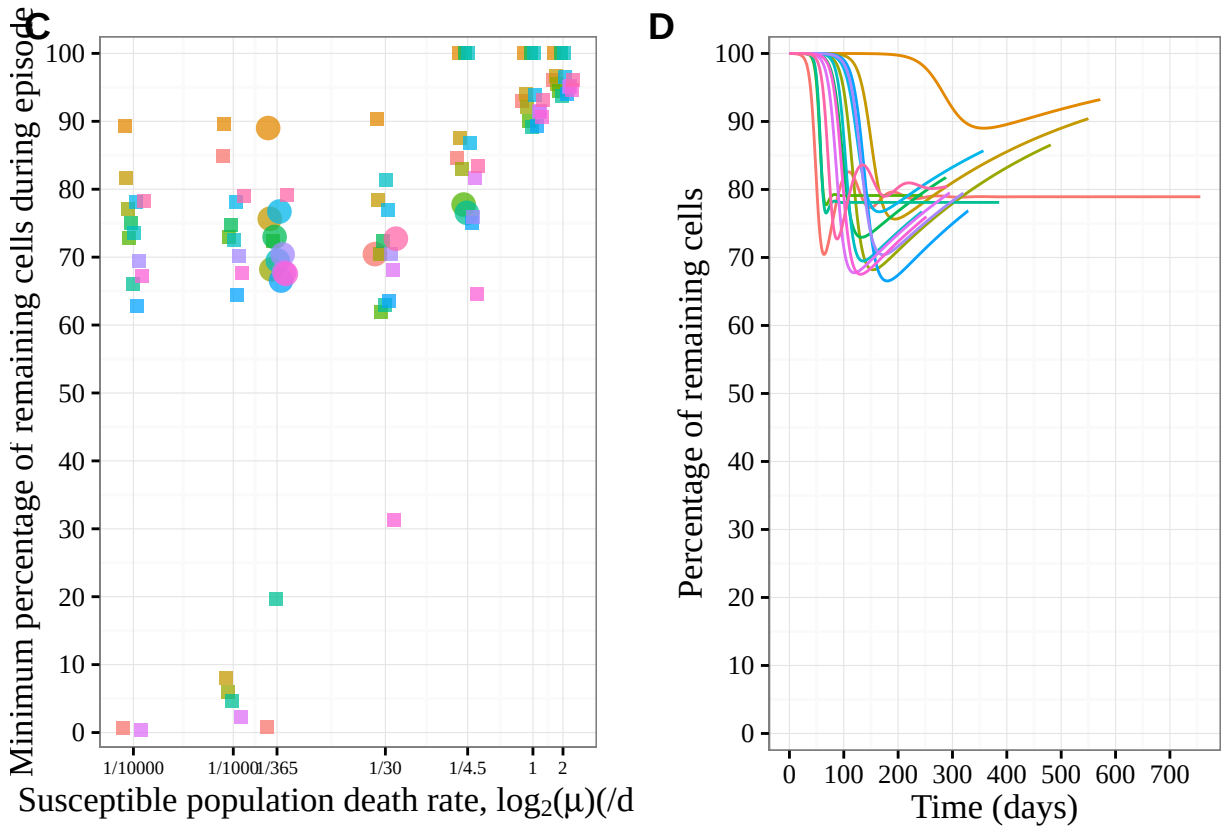


Figure 6: total epithelial cell loss during infection. A) minimum remaining at some point of infection across all mus; B) time series of cell loss among best fits only